

FIGURE 1

CGTCCTATCTGCAGTCGGCTACTTTTCAGTGGCAGAAGAGGCCACATCTGCTTCCTGTAGG
CCCTCTGGGCAGAAGCA**ATG**CGCTGGTGTCTCCTCCTGATCTGGGCCCAGGGGCTGAGGCA
GGCTCCCCTCGCCTCAGGAATGATGACAGGCCAATAGAAACAACGGGGAACATTTCTGC
AGAGAAAGGTGGCTCTATCATCTTACAATGTCACCTCTCCTCCACCA CGGCACAAGTGAC
CCAGGTCAACTGGGAGCAGCAGGACCAGCTTCTGGCCATTTGTAATG CTGACTTGGGGTG
GCACATCTCCCCATCCTTCAAGGATCGAGTGGCCCCAGGTCCCGGCC TGGGCCTCACCT
CCAGTCGCTGACCGTGAACGATACAGGGGAGTACTTCTGCATCTATCACACCTACCCTGA
TGGGACGTACACTGGGAGAATCTTCCTGGAGGTCCTAGAAAGCTCAGTGGCTGAGCACGG
TGCCAGGTTCAGATTCCATTGCTTGGAGCCATGGCCGCGACGCTGGTGGTCATCTGCAC
AGCAGTCATCGTGGTGGTCGCGTTGACTAGAAAGAAGAAAGCCCTCAGAATCCATTCTGT
GGAAGGTGACCTCAGGAGAAAATCAGCTGGACAGGAGGAATGGAGCC CCAGTGCTCCCTC
ACCCCAAGGAAGCTGTGTCCAGGCAGAAGCTGCACCTGCTGGGCTCTGTGGAGAGCAGCG
GGGAGAGGACTGTGCCGAGCTGCATGACTACTTCAATGTCCTGAGTTACAGAAGCCTGGG
TAACTGCAGCTTCTTCA CAGAGACTGGT**TAG**CAACCAGAGGCATCTTCTGG

FIGURE 2

MRWCLLLIWAQGLRQAPLASGMMTGTIETTGNI~~SAEK~~GGSIILQCHLSSTTAQVTQVNWE
QQDQLLAICNADLGWHISPSFKDRVAPGPGGLGLTLQSLTVNDTGEYFCIYHTYPDGTYTG
RIFLEVL~~ESSVAEHGARFQI~~PLLGAMAATLVVICTAVIVVVALTRKKKALRIHSVEGDLR
RKSAGQEEWSPSAPSPPGSCVQAEAAPAGLCGEQRGEDCAELHDYFNVLSYRSLGNC~~SFF~~
TETG

Signal sequence

1-15

Transmembrane domain

140-160

N-glycosylation site.

32-35

101-104

236-239

cAMP- and cGMP-dependent protein kinase phosphorylation site.

180-183

N-myristoylation site.

21-26

25-30

31-36

90-95

116-121

144-149

Immunoglobulin domain

38-110

ITIM domain

218-228

FIGURE 3

GCCAGTTTCAGTTGGAGGAGAGGCCACATCCACTTTGCTGTAGGCCTCTGGTTAGAAGCA
TGCATGGCTGGCTGCTCCTGGTCTGGGTCCAGGGGCTGATACAGGCTGCCTTCCTCGCTA
CAGGAGCCACAGCAGGCACGATAGATACAAAGAGGAACATCTCTGCA GAGGAAGGTGGCT
CTGTCATCTTACAGTGTCACTTCTCCTCTGACACAGCTGAAGTGACC CAAGTCGACTGGA
AGCAGCAGGACCAGCTTCTGGCCATTTATAGTGTTGACCTGGGGTGG CATGTCGCTTCAG
TCTTCAGTGATCGGGTGGTCCCAGGCCCCAGCCTAGGCCTCACCTTC CAGTCTCTGACAA
TGAATGACACGGGAGAGTACTTCTGTACCTATCATACTATCCTGGTGGGATTTACAAGG
GGAGAATATTCTGAAGGTCCAAGAAAGCTCAGTGGCTCAGTTCCAGACTGCCCCGCTTG
GAGGAACCATGGCTGCTGTGCTGGGACTCATTTGCTTAATGGTCACAGGAGTGA CTGTAC
TGGCTAGAAAGAAGTCTATTAGAAATGCATTCTATAGAAAGTGGCCTTGGGAGAACAGAAG
CGGAGCCACAGGAATGGAACCTGAGGAGTCTCTCATCCCCTGGAAGC CCGTCCAGACAC
AAACTGCCCCCTGCTGGTCCCTGTGGAGAGCAGGCAGAAAGATGACTATGCTGACCCACAGG
AATACTTTAATGTCTGAGCTACAGAAGCCTAGAGAGCTTCATTGCTGTATCGAAGACTG
GCT**AA**CGACAGCTCTCTATCCCTCTCCCTATGTCTCTCTCTCTGTCTCTCTCTGTCTCTC
TCTGTCTCTGTCTCTGTCTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTGTGTGTGTG
TGTGTGTATGTGTGTATACATCATTAATGTTTCATTAACTAACTGCATATGGTGGAGGA
CCAGGAAATAAAAGTTTGTGTTGCTAATAAAATTAAGTGCTAACTT

FIGURE 4

MHGWLLL VVWQGLIQAAFLATGATAGTIDTKRNISAEEGGSVILQCHFSSDTAEVTQVDW
KQQDQLLAIYSVDLGWHVASVFSDRVVPGPSLGLTFQSLTMNDTGEYFCTYHTYPGGIYK
GRIFLKVQESSVAQFQTAPLGGTMAAVLGLICLMVTGVTVLARKKSI RMHSI ESGLGRTE
AEPQEWNLRLSSLSPGSPVQTQTAPAGPCGEQAEDDYADPQEYFNVLS YRSLESFIAVSKT
G

Signal sequence

1-16

Transmembrane domain

138-158

N-glycosylation site.

33-36

102-105

Glycosaminoglycan attachment site.

174-177

cAMP- and cGMP-dependent protein kinase phosphorylation site.

163-166

N-myristoylation site.

12-17

22-27

26-31

117-122

141-146

142-147

175-180

Immunoglobulin domain

39-111

ITIM domain

221-230